



SEQUENCE LISTING

<110> Russell, William
Klaenhammer, Todd

<120> LACTOBACILLUS BETA-GLUCURONIDASE AND DNA ENCODING THE SAME

<130> 5051.514DV

<140> US 10/673,935

<141> 2003-09-29

<150> US 09/862,660

<151> 2001-05-21

<150> US 60/206372

<151> 2000-05-23

<160> 14

<170> PatentIn version 3.2

<210> 1

<211> 2150

<212> DNA

<213> Lactobacillus gasseri

<220>

<221> CDS

<222> (153)..(1946)

<400> 1

tcctttctta attattctct ataaataaaa taaactgtga cgcgagggtta cagtcaaggg 60

atttaattta ttaaaccatt ttcaaatacta ttactctcc ccaagcgtaa aatatagata 120

agagaaaaca ttactagaaa ggaaaatcat ct atg gaa tct gca cta tat cca 173

Met Glu Ser Ala Leu Tyr Pro

1 5

att caa aat aaa tat cgg ttt aac act tta atg aat ggc act tgg caa 221

Ile Gln Asn Lys Tyr Arg Phe Asn Thr Leu Met Asn Gly Thr Trp Gln

10 15 20

ttt gaa act gat cct aac tct gtt ggt ctt gac gag gga tgg aat aaa 269

Phe Glu Thr Asp Pro Asn Ser Val Gly Leu Asp Glu Gly Trp Asn Lys

25 30 35

gag ttg cct gat cct gaa gaa atg cct gta cca ggt acg ttt gca gaa 317

Glu Leu Pro Asp Pro Glu Glu Met Pro Val Pro Gly Thr Phe Ala Glu

40 45 50 55

tta act act aag cga gac cgt aaa tac tat act gga gac ttt tgg tat 365

Leu Thr Thr Lys Arg Asp Arg Lys Tyr Tyr Thr Gly Asp Phe Trp Tyr

60 65 70

caa aaa gac ttc ttt att cct tca ttt cta aag aag aaa gaa ctt tat 413

Gln Lys Asp Phe Phe Ile Pro Ser Phe Leu Lys Lys Lys Glu Leu Tyr

75 80 85

atc cgt ttt ggt tct gtt act cat cgc gca aaa gta ttt att aat gga Ile Arg Phe Gly Ser Val Thr His Arg Ala Lys Val Phe Ile Asn Gly 90 95 100	461
cat gaa gtc ggt caa cat gaa ggt ggt ttt tta cca ttt caa gta aaa His Glu Val Gly Gln His Glu Gly Gly Phe Leu Pro Phe Gln Val Lys 105 110 115	509
att tca aat tat att aat tac gac caa act aat cgt gta act gtt tta Ile Ser Asn Tyr Ile Asn Tyr Asp Gln Thr Asn Arg Val Thr Val Leu 120 125 130 135	557
gtc aat aac gaa tta tct gaa aaa gct att cct tgc ggc acc gaa gaa Val Asn Asn Glu Leu Ser Glu Lys Ala Ile Pro Cys Gly Thr Glu Glu 140 145 150	605
atc tta gat aac ggt caa aaa ctt gct caa cct tat ttt gat ttc ttc Ile Leu Asp Asn Gly Gln Lys Leu Ala Gln Pro Tyr Phe Asp Phe Phe 155 160 165	653
aat tat tct ggc att atg cgg aat gtc tgg ctc tta gca ctt cct caa Asn Tyr Ser Gly Ile Met Arg Asn Val Trp Leu Leu Ala Leu Pro Gln 170 175 180	701
agc caa atc act aat ttt aaa cta aat tat caa tta gca aat aat aag Ser Gln Ile Thr Asn Phe Lys Leu Asn Tyr Gln Leu Ala Asn Asn Lys 185 190 195	749
gca aca att acc tac aat atc gag gca aat aat aat gct gaa ttt aaa Ala Thr Ile Thr Tyr Asn Ile Glu Ala Asn Asn Asn Ala Glu Phe Lys 200 205 210 215	797
gta aca ctt ttc gat aat caa aaa gaa gta gcg tgt gct act tct aaa Val Thr Leu Phe Asp Asn Gln Lys Glu Val Ala Cys Ala Thr Ser Lys 220 225 230	845
aat act agt agt tta aca att aag aat ccg cac ctt tgg agt cca aac Asn Thr Ser Ser Leu Thr Ile Lys Asn Pro His Leu Trp Ser Pro Asn 235 240 245	893
gat ccg tat tca tac aaa ata aag att gaa atg ctc gaa gac gga aaa Asp Pro Tyr Ser Tyr Lys Ile Lys Ile Glu Met Leu Glu Asp Gly Lys 250 255 260	941
aca gtt gac gaa tac aca gat aaa att ggt atc cgc aca gtt aaa att Thr Val Asp Glu Tyr Thr Asp Lys Ile Gly Ile Arg Thr Val Lys Ile 265 270 275	989
gtg aat gat aaa atc ttg ctc aat aat cac cca att tat tta aaa ggc Val Asn Asp Lys Ile Leu Leu Asn Asn His Pro Ile Tyr Leu Lys Gly 280 285 290 295	1037
ttt ggc aag cac gaa gat ttt aat gtt tta ggc aaa gca gtt aac gaa Phe Gly Lys His Glu Asp Phe Asn Val Leu Gly Lys Ala Val Asn Glu 300 305 310	1085
agc att atc aaa cgc gac tac gaa tgc atg aaa tgg att ggc gct aac Ser Ile Ile Lys Arg Asp Tyr Glu Cys Met Lys Trp Ile Gly Ala Asn 315 320 325	1133
tgt ttt aga agc agt cac tat cct tac gcc gaa gaa tgg tat caa tat	1181

Cys	Phe	Arg	Ser	Ser	His	Tyr	Pro	Tyr	Ala	Glu	Glu	Trp	Tyr	Gln	Tyr		
		330					335					340					
gcc	gat	aaa	tat	ggc	ttt	tta	att	att	gat	gaa	gta	ccc	gct	gtt	ggc	1229	
Ala	Asp	Lys	Tyr	Gly	Phe	Leu	Ile	Ile	Asp	Glu	Val	Pro	Ala	Val	Gly		
	345					350				355							
ctt	aat	cgt	tca	ata	act	aac	ttt	ctt	aat	gta	act	aat	tct	aat	cag	1277	
Leu	Asn	Arg	Ser	Ile	Thr	Asn	Phe	Leu	Asn	Val	Thr	Asn	Ser	Asn	Gln		
360					365					370					375		
tcg	cac	ttt	ttt	gct	tcg	aaa	act	gtg	cct	gaa	tta	aaa	aag	gtc	cat	1325	
Ser	His	Phe	Phe	Ala	Ser	Lys	Thr	Val	Pro	Glu	Leu	Lys	Lys	Val	His		
			380						385					390			
gaa	caa	gaa	ata	aaa	gaa	atg	atc	gat	cgc	gac	cag	cgt	cac	cct	tca	1373	
Glu	Gln	Glu	Ile	Lys	Glu	Met	Ile	Asp	Arg	Asp	Gln	Arg	His	Pro	Ser		
			395					400					405				
gtg	att	gcc	tgg	agt	tta	ttc	aat	gaa	cca	gaa	tca	act	act	caa	gaa	1421	
Val	Ile	Ala	Trp	Ser	Leu	Phe	Asn	Glu	Pro	Glu	Ser	Thr	Thr	Gln	Glu		
	410						415					420					
tcc	tat	gac	tat	ttc	aaa	gat	att	ttt	gcc	ttt	gcg	aga	aaa	ttg	gat	1469	
Ser	Tyr	Asp	Tyr	Phe	Lys	Asp	Ile	Phe	Ala	Phe	Ala	Arg	Lys	Leu	Asp		
	425					430					435						
cca	caa	aat	cgt	cct	tat	act	gga	act	tta	gtt	atg	ggc	agc	ggc	cca	1517	
Pro	Gln	Asn	Arg	Pro	Tyr	Thr	Gly	Thr	Leu	Val	Met	Gly	Ser	Gly	Pro		
440					445					450					455		
aaa	gtg	gat	aag	ctt	cac	cca	ctt	tgt	gac	ttt	gtc	tgc	tta	aac	cgt	1565	
Lys	Val	Asp	Lys	Leu	His	Pro	Leu	Cys	Asp	Phe	Val	Cys	Leu	Asn	Arg		
				460					465					470			
tat	tat	ggc	tgg	tac	gtt	gct	ggc	ggc	cct	gaa	atc	gtt	aat	gct	aaa	1613	
Tyr	Tyr	Gly	Trp	Tyr	Val	Ala	Gly	Gly	Pro	Glu	Ile	Val	Asn	Ala	Lys		
			475					480					485				
aag	atg	ctg	gaa	gat	gaa	cta	gac	ggc	tgg	caa	aac	tta	aag	ctt	aat	1661	
Lys	Met	Leu	Glu	Asp	Glu	Leu	Asp	Gly	Trp	Gln	Asn	Leu	Lys	Leu	Asn		
	490						495					500					
aaa	cca	ttt	gtc	ttt	act	gag	ttt	ggc	gct	gat	aca	tta	tct	tct	tct	1709	
Lys	Pro	Phe	Val	Phe	Thr	Glu	Phe	Gly	Ala	Asp	Thr	Leu	Ser	Ser	Ser		
	505					510					515						
cat	cgc	ctt	cca	gat	gaa	atg	tgg	agc	caa	gaa	tat	caa	aat	gaa	tat	1757	
His	Arg	Leu	Pro	Asp	Glu	Met	Trp	Ser	Gln	Glu	Tyr	Gln	Asn	Glu	Tyr		
	520				525					530					535		
tat	caa	atg	tat	ttt	gat	ata	ttt	aag	aaa	tat	cca	ttt	att	tgt	ggc	1805	
Tyr	Gln	Met	Tyr	Phe	Asp	Ile	Phe	Lys	Lys	Tyr	Pro	Phe	Ile	Cys	Gly		
				540					545					550			
gaa	tta	gtt	tgg	aac	ttt	gct	gac	ttt	aag	acg	agt	gaa	gga	atc	atg	1853	
Glu	Leu	Val	Trp	Asn	Phe	Ala	Asp	Phe	Lys	Thr	Ser	Glu	Gly	Ile	Met		
			555					560					565				
cgt	gtt	ggc	ggc	aac	gat	aaa	gga	att	ttt	act	cgc	gat	cgt	gaa	cct	1901	
Arg	Val	Gly	Gly	Asn	Asp	Lys	Gly	Ile	Phe	Thr	Arg	Asp	Arg	Glu	Pro		

570	575	580	
aaa gat att gcc ttt acc ttg aaa aag aga tgg	caa caa tta aat	1946	
Lys Asp Ile Ala Phe Thr Leu Lys Lys Arg Trp	Gln Gln Leu Asn		
585	590	595	
taatatttta gtttttacaa ataatcgtgc tcaattaaaa	ataatcgata tcatttttagt	2006	
tcatttgata tcgattatatt gattatgggc gcgatttttt	attgatttttg ataataattt	2066	
ctaactaaga aatgtttcat taatttatga aactaatatc	ttgtttctta aacaaatcat	2126	
atacaactaa gtctgatgaa tcca		2150	
<210> 2			
<211> 598			
<212> PRT			
<213> Lactobacillus gasseri			
<400> 2			
Met Glu Ser Ala Leu Tyr Pro Ile Gln Asn Lys Tyr Arg Phe Asn Thr			
1	5	10	
Leu Met Asn Gly Thr Trp Gln Phe Glu Thr Asp Pro Asn Ser Val Gly			
	20	30	
Leu Asp Glu Gly Trp Asn Lys Glu Leu Pro Asp Pro Glu Glu Met Pro			
	35	45	
Val Pro Gly Thr Phe Ala Glu Leu Thr Thr Lys Arg Asp Arg Lys Tyr			
	50	60	
Tyr Thr Gly Asp Phe Trp Tyr Gln Lys Asp Phe Phe Ile Pro Ser Phe			
65	70	80	
Leu Lys Lys Lys Glu Leu Tyr Ile Arg Phe Gly Ser Val Thr His Arg			
	85	95	
Ala Lys Val Phe Ile Asn Gly His Glu Val Gly Gln His Glu Gly Gly			
	100	110	
Phe Leu Pro Phe Gln Val Lys Ile Ser Asn Tyr Ile Asn Tyr Asp Gln			
	115	125	
Thr Asn Arg Val Thr Val Leu Val Asn Asn Glu Leu Ser Glu Lys Ala			
	130	140	
Ile Pro Cys Gly Thr Glu Glu Ile Leu Asp Asn Gly Gln Lys Leu Ala			
145	150	160	

Gln Pro Tyr Phe Asp Phe Phe Asn Tyr Ser Gly Ile Met Arg Asn Val
 165 170 175

Trp Leu Leu Ala Leu Pro Gln Ser Gln Ile Thr Asn Phe Lys Leu Asn
 180 185 190

Tyr Gln Leu Ala Asn Asn Lys Ala Thr Ile Thr Tyr Asn Ile Glu Ala
 195 200 205

Asn Asn Asn Ala Glu Phe Lys Val Thr Leu Phe Asp Asn Gln Lys Glu
 210 215 220

Val Ala Cys Ala Thr Ser Lys Asn Thr Ser Ser Leu Thr Ile Lys Asn
 225 230 235 240

Pro His Leu Trp Ser Pro Asn Asp Pro Tyr Ser Tyr Lys Ile Lys Ile
 245 250 255

Glu Met Leu Glu Asp Gly Lys Thr Val Asp Glu Tyr Thr Asp Lys Ile
 260 265 270

Gly Ile Arg Thr Val Lys Ile Val Asn Asp Lys Ile Leu Leu Asn Asn
 275 280 285

His Pro Ile Tyr Leu Lys Gly Phe Gly Lys His Glu Asp Phe Asn Val
 290 295 300

Leu Gly Lys Ala Val Asn Glu Ser Ile Ile Lys Arg Asp Tyr Glu Cys
 305 310 315 320

Met Lys Trp Ile Gly Ala Asn Cys Phe Arg Ser Ser His Tyr Pro Tyr
 325 330 335

Ala Glu Glu Trp Tyr Gln Tyr Ala Asp Lys Tyr Gly Phe Leu Ile Ile
 340 345 350

Asp Glu Val Pro Ala Val Gly Leu Asn Arg Ser Ile Thr Asn Phe Leu
 355 360 365

Asn Val Thr Asn Ser Asn Gln Ser His Phe Phe Ala Ser Lys Thr Val
 370 375 380

Pro Glu Leu Lys Lys Val His Glu Gln Glu Ile Lys Glu Met Ile Asp
 385 390 395 400

Arg Asp Gln Arg His Pro Ser Val Ile Ala Trp Ser Leu Phe Asn Glu
405 410 415

Pro Glu Ser Thr Thr Gln Glu Ser Tyr Asp Tyr Phe Lys Asp Ile Phe
420 425 430

Ala Phe Ala Arg Lys Leu Asp Pro Gln Asn Arg Pro Tyr Thr Gly Thr
435 440 445

Leu Val Met Gly Ser Gly Pro Lys Val Asp Lys Leu His Pro Leu Cys
450 455 460

Asp Phe Val Cys Leu Asn Arg Tyr Tyr Gly Trp Tyr Val Ala Gly Gly
465 470 475 480

Pro Glu Ile Val Asn Ala Lys Lys Met Leu Glu Asp Glu Leu Asp Gly
485 490 495

Trp Gln Asn Leu Lys Leu Asn Lys Pro Phe Val Phe Thr Glu Phe Gly
500 505 510

Ala Asp Thr Leu Ser Ser Ser His Arg Leu Pro Asp Glu Met Trp Ser
515 520 525

Gln Glu Tyr Gln Asn Glu Tyr Tyr Gln Met Tyr Phe Asp Ile Phe Lys
530 535 540

Lys Tyr Pro Phe Ile Cys Gly Glu Leu Val Trp Asn Phe Ala Asp Phe
545 550 555 560

Lys Thr Ser Glu Gly Ile Met Arg Val Gly Gly Asn Asp Lys Gly Ile
565 570 575

Phe Thr Arg Asp Arg Glu Pro Lys Asp Ile Ala Phe Thr Leu Lys Lys
580 585 590

Arg Trp Gln Gln Leu Asn
595

<210> 3

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide primer

<400> 3

agtcagatct acagctccag atcgattcac 30

<210> 4
 <211> 30
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide primer

<400> 4
 agtcgctagc ttacgaactg gcacagatgg 30

<210> 5
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide primer

<400> 5
 agtcagatct ttaatgcgcc gctacagg 28

<210> 6
 <211> 33
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide primer

<400> 6
 agtcgctagc aatgcagcag ctggcacgac agg 33

<210> 7
 <211> 32
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide primer

<400> 7
 agagtcgact aatgaagctt gttttgtttc ag 32

<210> 8
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide primer

<400> 8
 actgaattct tctttagtta atggctcag 29

<210> 9
 <211> 29
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic oligonucleotide primer

 <400> 9
 gtcgaattct actagaaagg aaaatcatc 29

<210> 10
 <211> 29
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic oligonucleotide primer

 <400> 10
 tgctctagat aattgagcac gattatttg 29

<210> 11
 <211> 30
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic oligonucleotide primer

 <400> 11
 agtccatgga atctgcacta tatccaattc 30

<210> 12
 <211> 30
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic oligonucleotide primer

 <400> 12
 actggaattc taattgagca cgattatttg 30

<210> 13
 <211> 20
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic oligonucleotide primer - GUS-1F

 <400> 13
 acagttgcga atacacagat 20

<210> 14
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide primer - GUS-1R

<400> 14
aggcgatgag aagaagataa tg

22